

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/685, 258 B
Source: IFWO
Date Processed by STIC: 05/22/2006

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IFWO

RAW SEQUENCE LISTING

DATE: 05/22/2006

PATENT APPLICATION: US/10/685,258B

TIME: 11:56:27

Input Set : A:\34132b.txt

Output Set: N:\CRF4\05222006\J685258B.raw

3 <110> APPLICANT: Carr, Antony M.
 5 <120> TITLE OF INVENTION: Cell-Cycle Checkpoint Genes
 7 <130> FILE REFERENCE: 27866/34132
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/685,258B
 C--> 11 <141> CURRENT FILING DATE: 2003-10-14
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB96/02197
 16 <151> PRIOR FILING DATE: 1996-09-06
 19 <150> PRIOR APPLICATION NUMBER: GB 9518220.0
 21 <151> PRIOR FILING DATE: 1995-09-06
 24 <160> NUMBER OF SEQ ID NOS: 14
 26 <170> SOFTWARE: PatentIn Ver. 3.1
 29 <210> SEQ ID NO: 1
 31 <211> LENGTH: 8239
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (80)..(8011)
 41 <400> SEQUENCE: 1
 42 ggcgtcttcc ggcagcggta cggtttggaga cgccgggaac ccgcgttggc gtgggttgact 60
 43 agtgcctcgc agcctcagc atg ggg gaa cat ggc ctg gag ctg gct tcc atg 112
 44 Met Gly Glu His Gly Leu Glu Leu Ala Ser Met
 45 1 5 10
 46 atc ccc gcc ctg cgg gag ctg ggc agt gcc aca cca gag gaa tat aat 160
 47 Ile Pro Ala Leu Arg Glu Leu Gly Ser Ala Thr Pro Glu Glu Tyr Asn
 48 15 20 25
 49 aca gtt gta cag aag cca aga caa att ctg tgt caa ttc att gac cgg 208
 50 Thr Val Val Gln Lys Pro Arg Gln Ile Leu Cys Gln Phe Ile Asp Arg
 51 30 35 40
 52 ata ctt aca gat gta aat gtt gtt gct gta gaa ctt gta aag aaa act 256
 53 Ile Leu Thr Asp Val Asn Val Val Ala Val Glu Leu Val Lys Lys Thr
 54 45 50 55
 55 gac tct cag cca acc tcc gtg atg ttg ctt gat ttc atc cag cat atc 304
 56 Asp Ser Gln Pro Thr Ser Val Met Leu Leu Asp Phe Ile Gln His Ile
 57 60 65 70 75
 58 atg aaa tcc tcc cca ctt atg ttt gta aat gtg agt gga agc cat gag 352
 59 Met Lys Ser Ser Pro Leu Met Phe Val Asn Val Ser Gly Ser His Glu
 60 80 85 90
 61 cgc aaa ggc agt tgt att gaa ttc agt aat tgg atc ata acg aga ctt 400
 62 Arg Lys Gly Ser Cys Ile Glu Phe Ser Asn Trp Ile Ile Thr Arg Leu
 63 95 100 105
 64 ctg cgg att gca gca act ccc tcc tgt cat ttg tta cac aag aaa atc 448
 65 Leu Arg Ile Ala Ala Thr Pro Ser Cys His Leu Leu His Lys Lys Ile

(pg-6)

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67	tgt gaa gtc atc tgt tca tta tta ttt ctt ttt aaa agc aag agt cct	496		
68	Cys Glu Val Ile Cys Ser Leu Leu Phe Leu Phe Lys Ser Lys Ser Pro			
69	125	130	135	
70	gct att ttt ggg gta ctc aca aaa gaa tta tta caa ctt ttt gaa gac	544		
71	Ala Ile Phe Gly Val Leu Thr Lys Glu Leu Leu Gln Leu Phe Glu Asp			
72	140	145	150	155
73	ttg gtt tac ctc cat aga aga aat gtg atg ggt cat gct gtg gaa tgg	592		
74	Leu Val Tyr Leu His Arg Arg Asn Val Met Gly His Ala Val Glu Trp			
75	160	165	170	
76	cca gtg gtc atg agc cga ttt tta agt caa tta gat gaa cac atg gga	640		
77	Pro Val Val Met Ser Arg Phe Leu Ser Gln Leu Asp Glu His Met Gly			
78	175	180	185	
79	tat tta caa tca gct cct ttg cag ttg atg agt atg caa aat tta gaa	688		
80	Tyr Leu Gln Ser Ala Pro Leu Gln Leu Met Ser Met Gln Asn Leu Glu			
81	190	195	200	
82	ttt att gaa gtc act tta tta atg gtt ctt act cgt att att gca att	736		
83	Phe Ile Glu Val Thr Leu Leu Met Val Leu Thr Arg Ile Ile Ala Ile			
84	205	210	215	
85	gtg ttt ttt aga agg caa gaa ctc tta ctt tgg cag ata ggt tgt gtt	784		
86	Val Phe Phe Arg Arg Gln Glu Leu Leu Leu Trp Gln Ile Gly Cys Val			
87	220	225	230	235
88	ctg cta gag tat ggt agt cca aaa att aaa tcc cta gca att agc ttt	832		
89	Leu Leu Glu Tyr Gly Ser Pro Lys Ile Lys Ser Leu Ala Ile Ser Phe			
90	240	245	250	
91	tta aca gaa ctt ttt cag ctt gga gga cta cca gca caa cca gct agc	880		
92	Leu Thr Glu Leu Phe Gln Leu Gly Gly Leu Pro Ala Gln Pro Ala Ser			
93	255	260	265	
94	act ttt ttc agc tca ttt ttg gaa tta tta aaa cac ctt gta gaa atg	928		
95	Thr Phe Phe Ser Ser Phe Leu Glu Leu Leu Lys His Leu Val Glu Met			
96	270	275	280	
97	gat act gac caa ttg aaa ctc tat gaa gag cca tta tca aag ctg ata	976		
98	Asp Thr Asp Gln Leu Lys Leu Tyr Glu Glu Pro Leu Ser Lys Leu Ile			
99	285	290	295	
100	aag aca cta ttt ccc ttt gaa gca gaa gct tat aga aat att gaa cct	1024		
101	Lys Thr Leu Phe Pro Phe Glu Ala Glu Ala Tyr Arg Asn Ile Glu Pro			
102	300	305	310	315
103	gtc tat tta aat atg ctg ctg gaa aaa ctc tgt gtc atg ttt gaa gac	1072		
104	Val Tyr Leu Asn Met Leu Leu Glu Lys Leu Cys Val Met Phe Glu Asp			
105	320	325	330	
106	ggt gtg ctc atg cgg ctt aag tct gat ttg cta aaa gca gct ttg tgc	1120		
107	Gly Val Leu Met Arg Leu Lys Ser Asp Leu Leu Lys Ala Ala Leu Cys			
108	335	340	345	
109	cat tta ctg cag tat ttc ctt aaa ttt gtg cca gct ggg tat gaa tct	1168		
110	His Leu Leu Gln Tyr Phe Leu Lys Phe Val Pro Ala Gly Tyr Glu Ser			
111	350	355	360	
112	gct tta caa gtc agg aag gtc tat gtg aga aat att tgt aaa gct ctt	1216		
113	Ala Leu Gln Val Arg Lys Val Tyr Val Arg Asn Ile Cys Lys Ala Leu			
114	365	370	375	

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115	ttg	gat	gtg	ctt	gga	att	gag	gta	gat	gca	gag	tac	ttg	ttg	ggc	cca	1264
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117	380					385					390					395	
118	ctt	tat	gca	gct	ttg	aaa	atg	gaa	agt	atg	gaa	atc	att	gag	gag	att	1312
119	Leu	Tyr	Ala	Ala	Leu	Lys	Met	Glu	Ser	Met	Glu	Ile	Ile	Glu	Glu	Ile	
120					400					405						410	
121	caa	tgc	caa	act	caa	cag	gaa	aac	ctc	agc	agt	aat	agt	gat	gga	ata	1360
122	Gln	Cys	Gln	Thr	Gln	Gln	Glu	Asn	Leu	Ser	Ser	Asn	Ser	Asp	Gly	Ile	
123				415					420						425		
124	tca	ccc	aaa	agg	cgt	cgt	ctc	agc	tcg	tct	cta	aac	cct	tct	aaa	aga	1408
125	Ser	Pro	Lys	Arg	Arg	Arg	Leu	Ser	Ser	Ser	Leu	Asn	Pro	Ser	Lys	Arg	
126			430					435					440				
127	gca	cca	aaa	cag	act	gag	gaa	att	aaa	cat	gtg	gac	atg	aac	caa	aag	1456
128	Ala	Pro	Lys	Gln	Thr	Glu	Glu	Ile	Lys	His	Val	Asp	Met	Asn	Gln	Lys	
129		445				450				455							
130	agc	ata	tta	tgg	agt	gca	ctg	aaa	cag	aaa	gct	gaa	tcc	ctt	cag	att	1504
131	Ser	Ile	Leu	Trp	Ser	Ala	Leu	Lys	Gln	Lys	Ala	Glu	Ser	Leu	Gln	Ile	
132	460					465				470						475	
133	tcc	ctt	gaa	tac	agt	ggc	cta	aag	aat	cct	gtt	att	gag	atg	tta	gaa	1552
134	Ser	Leu	Glu	Tyr	Ser	Gly	Leu	Lys	Asn	Pro	Val	Ile	Glu	Met	Leu	Glu	
135				480					485						490		
136	gga	att	gct	gtt	gtc	tta	caa	ctg	act	gct	ctg	tgt	act	gtt	cat	tgt	1600
137	Gly	Ile	Ala	Val	Val	Leu	Gln	Leu	Thr	Ala	Leu	Cys	Thr	Val	His	Cys	
138			495					500						505			
139	tct	cat	caa	aac	atg	aac	tgc	cgt	act	ttc	aag	gac	tgt	caa	cat	aaa	1648
140	Ser	His	Gln	Asn	Met	Asn	Cys	Arg	Thr	Phe	Lys	Asp	Cys	Gln	His	Lys	
141		510						515					520				
142	tcc	aag	aag	aaa	cct	tct	gta	gtg	ata	act	tgg	atg	tca	ttg	gat	ttt	1696
143	Ser	Lys	Lys	Lys	Pro	Ser	Val	Val	Ile	Thr	Trp	Met	Ser	Leu	Asp	Phe	
144		525					530					535					
145	tac	aca	aaa	gtg	ctt	aag	agc	tgt	aga	agt	ttg	tta	gaa	tct	gtt	cag	1744
146	Tyr	Thr	Lys	Val	Leu	Lys	Ser	Cys	Arg	Ser	Leu	Leu	Glu	Ser	Val	Gln	
147	540					545					550					555	
148	aaa	ctg	gac	ctg	gag	gca	acc	att	gat	aag	gtg	gtg	aaa	att	tat	gat	1792
149	Lys	Leu	Asp	Leu	Glu	Ala	Thr	Ile	Asp	Lys	Val	Val	Lys	Ile	Tyr	Asp	
150				560					565						570		
151	gct	ttg	att	tat	atg	caa	gta	aac	agt	tca	ttt	gaa	gat	cat	atc	ctg	1840
152	Ala	Leu	Ile	Tyr	Met	Gln	Val	Asn	Ser	Ser	Phe	Glu	Asp	His	Ile	Leu	
153			575					580						585			
154	gaa	gat	tta	tgt	ggg	atg	ctc	tca	ctt	cca	tgg	att	tat	tcc	cat	tct	1888
155	Glu	Asp	Leu	Cys	Gly	Met	Leu	Ser	Leu	Pro	Trp	Ile	Tyr	Ser	His	Ser	
156		590						595					600				
157	gat	gat	ggc	tgt	tta	aag	ttg	acc	aca	ttt	gcc	gct	aat	ctt	cta	aca	1936
158	Asp	Asp	Gly	Cys	Leu	Lys	Leu	Thr	Thr	Phe	Ala	Ala	Asn	Leu	Leu	Thr	
159		605				610					615						
160	tta	agc	tgt	agg	att	tca	gat	agc	tat	tca	cca	cag	gca	caa	tca	cga	1984
161	Leu	Ser	Cys	Arg	Ile	Ser	Asp	Ser	Tyr	Ser	Pro	Gln	Ala	Gln	Ser	Arg	
162	620					625					630					635	
163	tgt	gtg	ttt	ctt	ctg	act	ctg	ttt	cca	aga	aga	ata	ttc	ctt	gag	tgg	2032

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164 Cys Val Phe Leu Leu Thr Leu Phe Pro Arg Arg Ile Phe Leu Glu Trp
165                               640                               645                               650
166 aga aca gca gtt tac aac tgg gcc ctg cag agc tcc cat gaa gta atc 2080
167 Arg Thr Ala Val Tyr Asn Trp Ala Leu Gln Ser Ser His Glu Val Ile
168                               655                               660                               665
169 cgg gct agt tgt gtt agt gga ttt ttt atc tta ttg cag cag cag aat 2128
170 Arg Ala Ser Cys Val Ser Gly Phe Phe Ile Leu Leu Gln Gln Gln Asn
171                               670                               675                               680
172 tct tgt aac aga gtt ccc aag att ctt ata gat aaa gtc aaa gat gat 2176
173 Ser Cys Asn Arg Val Pro Lys Ile Leu Ile Asp Lys Val Lys Asp Asp
174                               685                               690                               695
175 tct gac att gtc aag aaa gaa ttt gct tct ata ctt ggt caa ctt gtc 2224
176 Ser Asp Ile Val Lys Lys Glu Phe Ala Ser Ile Leu Gly Gln Leu Val
177 700                               705                               710                               715
178 tgt act ctt cac ggc atg ttt tat ctg aca agt tct tta aca gaa cct 2272
179 Cys Thr Leu His Gly Met Phe Tyr Leu Thr Ser Ser Leu Thr Glu Pro
180                               720                               725                               730
181 ttc tct gaa cac gga cat gtg gac ctc ttc tgt agg aac ttg aaa gcc 2320
182 Phe Ser Glu His Gly His Val Asp Leu Phe Cys Arg Asn Leu Lys Ala
183                               735                               740                               745
184 act tct caa cat gaa tgt tca tct tct caa cta aaa gct tct gtc tgc 2368
185 Thr Ser Gln His Glu Cys Ser Ser Ser Gln Leu Lys Ala Ser Val Cys
186                               750                               755                               760
187 aag cca ttc ctt ttc cta ctg aaa aaa ata cct agt cca gta aaa 2416
188 Lys Pro Phe Leu Phe Leu Leu Lys Lys Lys Ile Pro Ser Pro Val Lys
189                               765                               770                               775
190 ctt gct ttc ata gat aat cta cat cat ctt tgt aag cat ctt gat ttt 2464
191 Leu Ala Phe Ile Asp Asn Leu His His Leu Cys Lys His Leu Asp Phe
192 780                               785                               790                               795
193 aga gaa gat gaa aca gat gta aaa gca gtt ctt gga act tta tta aat 2512
194 Arg Glu Asp Glu Thr Asp Val Lys Ala Val Leu Gly Thr Leu Leu Asn
195                               800                               805                               810
196 tta atg gaa gat cca gac aaa gat gtt aga gtg gct ttt agt gga aat 2560
197 Leu Met Glu Asp Pro Asp Lys Asp Val Arg Val Ala Phe Ser Gly Asn
198                               815                               820                               825
199 atc aag cac ata ttg gaa tcc ttg gac tct gaa gat gga ttt ata aag 2608
200 Ile Lys His Ile Leu Glu Ser Leu Asp Ser Glu Asp Gly Phe Ile Lys
201                               830                               835                               840
202 gag ctt ttt gtc tta aga atg aag gaa gca tat aca cat gcc caa ata 2656
203 Glu Leu Phe Val Leu Arg Met Lys Glu Ala Tyr Thr His Ala Gln Ile
204                               845                               850                               855
205 tca aga aat aat gag ctg aag gat acc ttg att ctt aca aca ggg gat 2704
206 Ser Arg Asn Asn Glu Leu Lys Asp Thr Leu Ile Leu Thr Thr Gly Asp
207 860                               865                               870                               875
208 att gga agg gcc gca aaa gga gat ttg gta cca ttt gca ctc tta cac 2752
209 Ile Gly Arg Ala Ala Lys Gly Asp Leu Val Pro Phe Ala Leu Leu His
210                               880                               885                               890
211 tta ttg cat tgt ttg tta tcc aag tca gca tct gtc tct gga gca gca 2800
212 Leu Leu His Cys Leu Leu Ser Lys Ser Ala Ser Val Ser Gly Ala Ala

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213          895          900          905
214 tac aca gaa att aga gct ctg gtt gca gct aaa agt gtt aaa ctg caa 2848
215 Tyr Thr Glu Ile Arg Ala Leu Val Ala Ala Lys Ser Val Lys Leu Gln
216          910          915          920
217 agt ttt ttc agc cag tat aag aaa ccc atc tgt cag ttt ttg gta gaa 2896
218 Ser Phe Phe Ser Gln Tyr Lys Lys Pro Ile Cys Gln Phe Leu Val Glu
219          925          930          935
220 tcc ctt cac tct agt cag atg aca gca ctt ccg aat act cca tgc cag 2944
221 Ser Leu His Ser Ser Met Thr Ala Leu Pro Asn Thr Pro Cys Gln
222 940          945          950          955
223 aat gct gac gtg cga aaa caa gat gtg gct cac cag aga gaa atg gct 2992
224 Asn Ala Asp Val Arg Lys Gln Asp Val Ala His Gln Arg Glu Met Ala
225          960          965          970
226 tta aat acg ttg tct gaa att gcc aac gtt ttc gac ttt cct gat ctt 3040
227 Leu Asn Thr Leu Ser Glu Ile Ala Asn Val Phe Asp Phe Pro Asp Leu
228          975          980          985
229 aat cgt ttt ctt act agg aca tta caa gtt cta cta cct gat ctt gct 3088
230 Asn Arg Phe Leu Thr Arg Thr Leu Gln Val Leu Leu Pro Asp Leu Ala
231          990          995          1000
232 gcc aaa gca agc cct gca gct tct gct ctc att cga act tta gga aaa 3136
233 Ala Lys Ala Ser Pro Ala Ala Ser Ala Leu Ile Arg Thr Leu Gly Lys
234          1005          1010          1015
235 caa tta aat gtc aat cgt aga gag att tta ata aac aac ttc aaa tat 3184
236 Gln Leu Asn Val Asn Arg Arg Glu Ile Leu Ile Asn Asn Phe Lys Tyr
237 1020          1025          1030          1035
238 att ttt tct cat ttg gtc tgt tct tgt tcc aaa gat gaa tta gaa cgt 3232
239 Ile Phe Ser His Leu Val Cys Ser Cys Ser Lys Asp Glu Leu Glu Arg
240          1040          1045          1050
241 gcc ctt cat tat ctg aag aat gaa aca gaa att gaa ctg ggg agc ctg 3280
242 Ala Leu His Tyr Leu Lys Asn Glu Thr Glu Ile Glu Leu Gly Ser Leu
243          1055          1060          1065
244 ttg aga caa gat ttc caa gga ttg cat aat gaa tta ttg ctg cgt att 3328
245 Leu Arg Gln Asp Phe Gln Gly Leu His Asn Glu Leu Leu Leu Arg Ile
246          1070          1075          1080
247 gga gaa cac tat caa cag gtt ttt aat ggt ttg tca ata ctt gcc tca 3376
248 Gly Glu His Tyr Gln Gln Val Phe Asn Gly Leu Ser Ile Leu Ala Ser
249          1085          1090          1095
250 ttt gca tcc agt gat gat cca tat cag ggc ccg aga gat atc ata tca 3424
251 Phe Ala Ser Ser Asp Asp Pro Tyr Gln Gly Pro Arg Asp Ile Ile Ser
252 1100          1105          1110          1115
253 cct gaa ctg atg gct gat tat tta caa ccc aaa ttg ttg ggc att ttg 3472
254 Pro Glu Leu Met Ala Asp Tyr Leu Gln Pro Lys Leu Leu Gly Ile Leu
255          1120          1125          1130
256 gct ttt ttt aac atg cag tta ctg agc tct agt gtt ggc att gaa gat 3520
257 Ala Phe Phe Asn Met Gln Leu Leu Ser Ser Ser Val Gly Ile Glu Asp
258          1135          1140          1145
259 aag aaa atg gcc ttg aac agt ttg atg tct ttg atg aag tta atg gga 3568
260 Lys Lys Met Ala Leu Asn Ser Leu Met Ser Leu Met Lys Leu Met Gly
261          1150          1155          1160

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 5,6,8

Seq#:14; Xaa Pos. 5

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

L:1873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0